

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Ronald M.
No, David

(ii) TITLE OF INVENTION: HORMONE-MEDIATED METHODS FOR MODULATING
EXPRESSION OF EXOGENOUS GENES IN MAMMALIAN SYSTEMS, AND
PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gray Cary Ware & Freidenrich LLP

(B) STREET: 4365 Executive Drive, Suite 1600

(C) CITY: San Diego

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 92121-2189

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/974,530

(B) FILING DATE: November 19, 1997

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.

(B) REGISTRATION NUMBER: 34,192

(C) REFERENCE/DOCKET NUMBER: SALK1520-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-677-1409

(B) TELEFAX: 619-677-1465

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
 1 5 10 15
 Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 35 40 45
 Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
 50 55 60
 Lys Cys Xaa Xaa Xaa Gly Met
 65 70

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Gly Cys Lys Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

09042488-031698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ser Cys Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2241
(D) OTHER INFORMATION: /product= "VgEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GCC CCC CCG ACC GAT CTC AGC CTG GCG GAC GAG CTC CAC TTA GAC 48
Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
1 5 10 15

GCG GAG GAC CTC GCG ATG CCG CAT GCG GAC GCG CTA GAC GAT TTC GAT 96
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
20 25 30

CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
35 40 45

CAC GAC TCC GCC CCC TAC GCG GCT CTG GAT ATG GCC GAC TTC GAG TTT 192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
50 55 60

GAG CAG ATG TTT ACC GAT GCG CTT GCA ATT GAC GAG TAC GGT GCG AAG 240
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
65 70 75 80

CTT CTA GGT ACC TCT AGA/AGG ATA TCG AAT TCT ATA TCT TCA GGT CCG 288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
85 90 95

GAT GAT CTC TCG CCT TCG AGC AGC TTG AAC GGA TAC TCG GCG AAC GAA 336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
100 105 110

AGC TGC GAT GCG AAG AAG AGC AAG AAG GGA CCT GCG CCA CCG CTC CAA 384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
115 120 125

031698 031698 031698

GAG GAG CTG TGC CTG GTT TGC GGC GAC AGG GCC TCC GGC TAC CAC TAC 432
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

AAC GCC CTC ACC TGT GGA TCC TGC AAG CTG TTC TTT CGA CGC AGC GTT 480
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
 145 150 155 160

ACG AAG AGC GCC CTC TAC TGC TGC AAG TTC GGG CGC GCC TGC GAA ATC 528
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

GAC ATG TAC ATG AGG CGA AAG TGT CAG GAG TGC CGC CTC AAA AAG TGC 576
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190

CTG GCC CTG GGT ATG CGC CGC GAA TGC CTC CTC CGC GAG AAC CAA TGT 624
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

GCG ATG AAG CGC CGC GAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATG 672
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

ACC ACT TCG CGC AGC TGT CAG CAT GCC GGC AAT GGC AGC TTG GCC TCT 720
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

GGT GCC GCC CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATG ACA 768
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

TGC GAG CGC CCC CAG CAT GCC ACT ATT CGC CCA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTG GCC AAG TGT CAA GCG CGC AAT ATA CCT TCC TTA ACG TAC AAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTG GCC GTT ATA TAC AAG TTA ATT TCG TAC CAG GAT GCC TAT GAG CAG 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATG AGT CAA CCC GAT GAG AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAG AGC CAA ACG GAC CTC AGC TTT CGC CAT ATA ACC GAG ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACC CTC CAG TTG ATT GTT GAG TTT GCT AAA GGT CTA CCA GCG TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

00042438 "031698

ACA AAG ATA CCC CAG GAG GAC CAG ATC ACG TTA CTA AAG GCC TGC TGC 1104
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TCG GAG CTC ATG ATG CTG CGT ATG GCA CGA CCG TAT GAC CAC AGC TCG 1152
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC GCG AAT AAT AGA TCA TAT ACG CGG CAT TCT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATG GCC GGA ATG GCT CAT AAC ATT GAA GAC CTC CTG CAT TTC TGC 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

CGC CAA ATG TTC TCG ATG AAG CTG GAC AAC CTC GAA TAC CGC CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

ACT GCC ATT GTG ATC TTC TCG GAC CGG CCG GGC CTG GAG AAG GCC CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Gln Lys Ala Gln
 435 440 445

CTA CTC GAA CGC ATC CAG AGC TAC TAC ATC GAC ACG CTA CGC ATT TAT 1392
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CGC CAC TGC GGC GAC TCA ATG AGC CTC CTC TTC TAC GCA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

AAG CTC CTC TCG ATC CTC ACC GAG CTG CTT ACG CTC GGC AAC CAG AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CGC AAA CTC CCC AAG 1536
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAG GAG ATC TGC GAC CTT CAT GCC ATC CGC CCA TCG CTC CAG 1584
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCG CAC CTT CAG ATT ACC CAG GAG GAG AAC CAG CGT CTC GAG CGG GCT 1632
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

GAG CGT ATG CGG GCA TCG CTT GGG GGC GCC ATT ACC GCC GGC ATT GAT 1680
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TGC GAC TCT GCC TCC ACT TCG GCG GCG GCA GCC GCG GCC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

03042438 031698

CCT CAG CTT CAG CCC CAG CCC CAA CCC TCC TCC CTG ACC CAG AAC GAT 1776
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAC CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CTT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTG CAA GGT CAA CTG CAA CCC CAG CTC CAA CCA CAG CTT CAG ACC CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC GTC TCC GCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

CCC GTG CCC GGC TCC GTA ACC GCA CCT GGT TCC TTG TCC GCG GTC AGT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACG AGC AGC GAA TAC ATG GGC GGA AGT GCG GCC ATA GGA CCC ATC ACG 2016
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

CCG GCA ACC ACC AGC AGT ATC ACG GCT GCC GTT ACC GCT AGC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA CCG GTA CCG ATG GGC AAC GGA GTT GCA GTC GGT GTT GCG CTC 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

GGC GGC AAC GTC ACC ATG TAT GCG AAC GCC CAG ACC GCG ATG GCC TTG 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG GGT GTA GCC CTG CAT TCG CAC CAA GAG CAG CTT ATC GCG GGA CTC 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

GCG GTT AAG TCG GAG CAC TCG ACC ACT GCA TAG 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

0316193 09042453

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
130 135 140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
180 185 190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
195 200 205

Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
290 295 300

05042433 031633

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
370 375 380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
385 390 395 400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
405 410 415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
420 425 430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
435 440 445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
450 455 460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
565 570 575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln

090424-031600

595 600 605
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..2241
 (D) OTHER INFORMATION: /product= "VpEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GCC CCC CCG ACC GAT GTC AGC CTG GCG GAC GAG CTC CAC TTA GAC 48
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15
 GCG GAG GAC CTG CCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT 96
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

09042488.031698

CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GCA TTT ACC CCC 144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
35 40 45

CAC GAC TCC GCC CCC TAC GGC GGT CTG GAT ATG GCC GAC TTC GAG TTT 192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
50 55 60

GAG CAG ATG TTT ACC GAT GCC CTT GCA ATT GAC GAG TAC GGT GGG AAG 240
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
65 70 75 80

CTT CTA GGT ACC TGT AGA AGG ATA TCG AAT TCT ATA TCT TCA GGT CCG 288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
85 90 95

GAT GAT CTC TCG CTT TCG AGC AGC TTG AAC GGA TAC TCG CCG AAC GAA 336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
100 105 110

AGC TGC GAT GCG AAG AAG AGC AAG AAG GGA CCT GCG CCA CCG CTG CAA 384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
115 120 125

GAG GAG CTG TGC CTG GTT TGC GGC GAC AGG GCG TCC GGC TAC CAC TAC 432
Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
130 135 140

AAC GCC CTC ACC TGT GAG GGC TGC AAG GCG TTC TTT CGA CCG AGC GTT 480
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
145 150 155 160

ACG AAG AGC GCC CTC TAC TGC TGC AAG TTC GCG CCG GCC TGC GAA ATG 528
Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
165 170 175

GAC ATG TAC ATG AGC CGA AAG TGT CAG GAG TGC CCG CTG AAA AAG TGC 576
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
180 185 190

CTG GCC CTG GGT ATG CCG CCG GAA TGC CTC CTC CCG GAG AAC CAA TGT 624
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
195 200 205

GCG ATG AAG CCG CCG CAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATG 672
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
210 215 220

ACC ACT TCG CCG AGC TCT CAG CAT GGC GGC AAT GGC AGC TTG CCG TCT 720
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
225 230 235 240

GCT GCG GCG CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATG ACA 768
Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
245 250 255

06042433 031600

TGC GAG CCG CCC CAG CAT GCC ACT ATT CCG CTA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTG GCC AAG TGT CAA GCG CCG AAT ATA CCT TCC TTA AGC TAC AAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTG CCC GTT ATA TAC AAG TTA ATT TGG TAC CAG CAT GCG TAT GAG CAG 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATG AGT CAA CCC GAT GAG AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAG AGC CAA ACG GAC CTC AGC TTT CCG CAT ATA ACC GAG ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACG CTC CAG TTG ATT GTT GAG TTT GCT AAA GGT CTA CCA GCG TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

ACA AAG ATA CCC CAG GAG GAC CAG ATC ACG TTA CTA AAG GCG TGC TCG 1104
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TCG GAG CTC ATG ATG CTG CGT ATG GCA CGA CCG TAT GAC CAC AGC TCG 1152
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC CCG AAT AAT AGA TCA TAT ACG CCG GAT TCT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATG CCC GGA ATG GCT GAT AAC ATT GAA GAC CTG CTG CAT TTC TGC 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

CCG CAA ATG TTC TCG ATG AAG GTG GAC AAC CTC GAA TAC CCG CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

ACT GCC ATT CTC ATC TTC TCG GAG CCG CCG GCG CTC GAG AAG GCC CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445

CTA GTC GAA GCG ATC CAG AGC TAC TAC ATC GAC ACG CTA CCG ATT TAT 1392
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CCG CAC TGC GCG GAC TCA ATG AGC CTC CTC TTC TAC GCA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

031698-034243

AAG CTG CTC TCG ATC CTC ACC GAG CTG CGT ACG CTG GGC AAC CAG AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

CCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CGC AAA CTG CCC AAG 1536
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAG GAG ATC TGG GAC GTT CAT GCC ATC CGC CCA TCG GTC CAG 1584
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCG CAC GTT CAG ATT ACC CAG GAG GAG AAC GAG CGT CTC GAG CGG GCT 1632
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540

GAG CGT ATG CGG GCA TCG GTT GGG GGC GCC ATT ACC GGC GCC ATT GAT 1680
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TGC GAC TCT GCC TCC ACT TCG GCG GCG GCA GCC GCG GCC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCC TCC TCC CTG ACC CAG AAC GAT 1776
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAC CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTG CAA GGT CAA CTG CAA CCC CAG CTC CAA CCA CAG GTT CAG ACG CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC GTT CCC GTC TCC GCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

CCC GTG CCC GCG TCC GTA ACC GCA CCT GGT TCC TTG TCC GCG GTC AGT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACG AGC AGC CAA TAC ATG GCG GGA AGT GCG GCC ATA GGA CCC ATC ACG 2016
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

CCG GCA ACC ACC AGC AGT ATC ACC GGT GCC GTT ACC GGT AGC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA GCG GTA CCG ATG GCG AAC GGA GTT GGA CTC GGT GTT GCG CTC 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

09042438 031636

GGC GGC AAC GTC AGC ATG TAT GCG AAC GCC CAG ACG GCG ATG GCC TTG 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG GGT GTA GCC CTG CAT TCG CAC CAA GAG CAG CTT ATC GCG GCA CTC 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

GCG GTT AAG TCG GAG CAC TCG ACG ACT GCA TAG 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met

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165 170 175
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

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Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
565 570 575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
595 600 605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
610 615 620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
625 630 635 640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
645 650 655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
705 710 715 720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala
740 745

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..3126
 (D) OTHER INFORMATION: /product= "GecR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC TCC AAA GAA TCA TTA ACT CCT GGT AGA GAA GAA AAC CCC AGC 48
 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 1 5 10 15

ACT CTG CTT GCT CAG CAG AGG GGA GAT CTG ATG GAC TTC TAT AAA ACC 96
 Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20 25 30

CTA AGA GGA GGA GCT ACT CTG AAG GTT TCT GCG TCT TCA CCC TCA CTC 144
 Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35 40 45

GCT CTC GCT TCT CAA TCA GAC TCC AAG CAG CGA AGA CTT TTG GTT GAT 192
 Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 50 55 60

TTT CCA AAA GGC TCA GTA AGC AAT GCG CAG CAG CCA GAT CTG TCC AAA 240
 Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 65 70 75 80

GCA GTT TCA CTC TCA ATG GGA CTG TAT ATG GGA CAG ACA GAA ACA AAA 288
 Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85 90 95

GTG ATG GGA AAT GAC CTG GGA TTC CCA CAG CAG GGC CAA ATC AGC CTT 336
 Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
 100 105 110

TCC TCG GGG GAA ACA GAC TTA AAG CTT TTG GAA GAA AGC ATT GCA AAC 384
 Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
 115 120 125

CTC AAT AGC TCG ACC AGT GTT CCA CAG AAC CCC AAG AGT TCA GCA TCC 432
 Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
 130 135 140

09042438 031698

ACT GCT GTG TCT GCT GCC CCC ACA GAG AAG GAG TTT CCA AAA ACT CAC 480
 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
 145 150 155 160

TCT GAT GTA TCT TCA GAA CAG CAA CAT TTG AAG GGC CAG ACT GGC ACC 528
 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
 165 170 175

AAC GGT GCC AAT GTG AAA TTG TAT ACC ACA GAC CAA AGC ACC TTT GAC 576
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
 180 185 190

ATT TTG CAG GAT TTG CAG TTT TCT TCT GGG TCC CCA GGT AAA GAG ACG 624
 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
 195 200 205

AAT GAG AGT CCT TGG AGA TCA GAC CTG TTG ATA GAT GAA AAC TGT TTG 672
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
 210 215 220

CTT TCT CCT CTG GCG GGA CAA GAC GAT TCA TTC CTT TTG GAA GGA AAC 720
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
 225 230 235 240

TCG AAT GAG GAC TGC AAG CCT CTC ATT TTA CCG GAC ACT AAA CCC AAA 768
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
 245 250 255

ATT AAG GAT AAT GCA GAT CTG GTT TTG TCA AGC CCG AGT AAT GTA ACA 816
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
 260 265 270

CTG CCC CAA GTG AAA ACA GAA AAA GAA GAT TTC ATC GAA CTC TGC ACC 864
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
 275 280 285

CCT GGG GTA ATT AAG CAA GAG AAA CTG GGC ACA GTT TAC TGT CAG GCA 912
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
 290 295 300

AGC TTT CCT GCA GCA AAT ATA ATT GGT AAT AAA ATG TCT GCC ATT TCT 960
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
 305 310 315 320

GTT CAT GGT GTG AGT ACC TCT GCA GGA CAG ATG TAC CAC TAT GAC ATG 1008
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
 325 330 335

AAT ACA GCA TCC CTT TCT CAA CAG CAG GAT CAG AAG CCT ATT TTT AAT 1056
 Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
 340 345 350

GTC ATT CCA CCA ATT CCC GTT GGT TCC GAA AAT TGC AAT AGC TGC CAA 1104
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Tyr Asn Arg Cys Gln
 355 360 365

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GGA TCT GGA GAT GAC AAC TTG ACT TCT CTG GGG ACT CTG AAC TTC CCT 1152
 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
 370 375 380

GGT CGA ACA GTT TTT TCT AAT GGC TAT TCA AGC CCC AGC ATG AGA CCA 1200
 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
 385 390 395 400

GAT GTA AGC TCT CCT CCA TCC AGC TCC TCA ACA GCA ACA ACA GGA CCA 1248
 Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
 405 410 415

CCT CCC AGC GGC CGC GTG CAA GAG GAG CTG TGC CTG GTT TGC GGC GAC 1296
 Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
 420 425 430

AGG GCC TCC GGC TAC CAC TAC AAC GCC CTC ACC TGT GGA TCC TGC AAG 1344
 Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
 435 440 445

CTG TTC TTT CGA CGC AGC GTT ACG AAG AGC GCC CTC TAC TGC TGC AAG 1392
 Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
 450 455 460

TTC GGG CGC GCC TGC GAA ATG GAC ATG TAC ATG AGG CGA AAG TGT CAG 1440
 Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
 465 470 475 480

GAG TGC CGC CTC AAA AAG TGC CTG GCC GTG GGT ATG CGG CGC GAA TGC 1488
 Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
 485 490 495

CTC CTC CGC GAG AAC CAA TGT CGC ATG AAG CGC CGC GAA AAG GCC 1536
 Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
 500 505 510

CAG AAG GAG AAG GAC AAA ATG ACC ACT TCG CGC AGC TCT CAG CAT GCC 1584
 Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
 515 520 525

GGC AAT GCC AGC TTG GCC TCT GGT GCC GGC CAA GAC TTT GTT AAG AAG 1632
 Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys
 530 535 540

GAG ATT CTT GAC CTT ATG ACA TGC GAG CGC CCC CAG CAT GCC ACT ATT 1680
 Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
 545 550 555 560

CCG CTA CTA CCT GAT GAA ATA TTG GCC AAG TGT CAA GCG CGC AAT ATA 1728
 Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
 565 570 575

CCT TCC TTA ACC TAC AAT CAG TTG GCG GTT ATA TAC AAG TTA ATT TGG 1776
 Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
 580 585 590

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TAC CAG GAT GGC TAT GAG CAG CCA TCT GAA GAG GAT CTC AGG CGT ATA	1824
Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile	
595 600 605	
ATG AGT CAA CCC GAT GAG AAC GAG AGC CAA ACG GAC CTC ACC TTT CCG	1872
Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg	
610 615 620	
CAT ATA ACC GAG ATA ACC ATA CTC ACG CTC CAG TTG ATT GTT GAG TTT	1920
His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe	
625 630 635 640	
GCT AAA GGT CTA CCA GCG TTT ACA AAG ATA CCC CAG GAG GAC CAG ATC	1968
Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile	
645 650 655	
ACG TTA CTA AAG GCC TGC TCG TCG CAG GTG ATG ATC CTC CGT ATG GCA	2016
Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg/Met Ala	
660 665 670	
CGA CGC TAT GAC CAC AGC TCG GAC TCA ATA TTC TTC GCG AAT AAT AGA	2064
Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg	
675 680 685	
TCA TAT ACG CGG GAT TCT TAC AAA ATG GCC GGA ATG GCT GAT AAC ATT	2112
Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile	
690 695 700	
GAA GAC CTG CTC CAT TTC TGC CGC CAA ATG TTG TCG ATC AAG CTC GAC	2160
Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp	
705 710 715 720	
AAC CTC CAA TAC GCG CTT CTC ACT GCC ATT GTG ATC TTC TCG GAC CGG	2208
Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg	
725 730 735	
CGG GCG CTG GAG AAG GCC CAA CTA CTC GAA GCG ATC CAG AGC TAC TAC	2256
Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr	
740 745 750	
ATC GAC ACG CTA CGC ATT TAT ATA CTC AAC CGC CAC TGC GGC GAC TCA	2304
Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser	
755 760 765	
ATG AGC CTC GTC TTC TAC GCA AAG CTG CTC TCG ATC CTC ACC GAG CTC	2352
Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu	
770 775 780	
CGT ACG CTG GCG AAC CAG AAC GCC GAG ATG TGT TTC TCA CTA AAG CTC	2400
Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu	
785 790 795 800	
AAA AAC CGC AAA CTG CCC AAG TTC CTC GAG GAG ATC TGG GAC GTT CAT	2448
Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His	
805 810 815	

GCG ATC CCG CCA TCG CTC CAG TCG CAC CTT CAG ATT ACC CAG GAG GAG 2496
 Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
 820 825 830

AAC GAG CGT CTC GAG CCG GCT GAG CGT ATG CCG GCA TCG GTT GCG CCG 2544
 Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
 835 840 845

GCG ATT ACC GCG GCG ATT CAT TCG CAG TCT GCG TCG ACT TCG GCG GCG 2592
 Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
 850 855 860

GCA GCG GCG GCG CAG CAT CAG CCT CAG CTT CAG CCG CAG CCG CAA CCG 2640
 Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
 865 870 875 880

TCG TCG CTC ACC CAG AAC GAT TCG CAG CAC CAG ACA CAG CCG CAG CTA 2688
 Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
 885 890 895

CAA CCT CAG CTA CCA CCT CAG CTC CAA GGT CAA CTC CAA CCG CAG CTC 2736
 Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
 900 905 910

CAA CCA CAG CTT CAG ACG CAA CTC CAG CCA CAG ATT CAA CCA CAG CCA 2784
 Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
 915 920 925

CAG CTC CTT CCG CTC TCG GCT CCG CTC CCG CCG TCG CTA ACC GCA CCT 2832
 Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
 930 935 940

GGT TCG TTG TCG CCG CTC AGT ACG ACC AGC GAA TAC ATG GCG GGA AGT 2880
 Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
 945 950 955 960

GCG GCG ATA GGA CCG ATC ACG CCG GCA ACC ACC AGC AGT ATC ACG GCT 2928
 Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
 965 970 975

GCG GTT ACC GCT AGC TCG ACC ACA TCA CCG GTA CCG ATG GCG AAC GGA 2976
 Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 980 985 990

GTT GGA CTC GGT GTT GCG CTC GCG GCG AAC CTC ACC ATG TAT CCG AAC 3024
 Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 995 1000 1005

GCG CAG ACG GCG ATG GCG TTG ATG GGT GTA GCG CTC CAT TCG CAC CAA 3072
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

CAG CAG CTT ATC GCG GGA CTC GCG GTT AAG TCG CAG CAC TCG ACC ACT 3120
 Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

09042453 031608

GCA TAG
Ala

3126

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1 5 10 15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180 185 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195 200 205

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Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Ile Cys Thr
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
405 410 415

Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
420 425 430

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
435 440 445

Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
450 455 460

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
465 470 475 480

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
485 490 495

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Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
500 505 510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Glu His Gly
515 520 525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys
530 535 540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
545 550 555 560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
565 570 575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
580 585 590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile
595 600 605

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg
610 615 620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
625 630 635 640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile
645 650 655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala
660 665 670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
675 680 685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
690 695 700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
705 710 715 720

Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
725 730 735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr
740 745 750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
755 760 765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu
770 775 780

09042488 031698

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu
785 790 795 800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
980 985 990

Val Gly Val Gly Val Gly Val Gly Asn Val Ser Met Tyr Ala Asn
995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
1010 1015 1020

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
1025 1030 1035 1040

Ala

090424183 031698

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"
/note= "N at position 7 is 0 up to 5 nucleotides, with 1 nucleotide being especially preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RGBNNMNTGN NCY

13

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"
/note= "N at position 7 can be 0 up to 5 nucleotides, with 1 nucleotide being preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RGNNCANKNN VCY

13

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

 03042433 031633
 3697E0 33424060

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACTGCANTGT TCT

13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: product = "Ecdysone Response Element"
/note = "N at position 7 can be 0 up to 5 nucleotides, with 3 nucleotides being preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

RCBNNMNRGB NNM

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACAACGGCC TCACCTGTGG ATCCTGCAAG GTGTTTCTTT CGACGCAGC

49

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

09042438 1031698

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTACTCCCGG GCGCGGGCTA TCGCGGGCGG GGGTAATCG TAGGGCGCGG GCA 53

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACTGCCCC GCGGCTAGCG ATTAGCGCG CCGGCATAG CCGCGCGCGG GCA 53

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGATCG ACAAGTCCAT TCTTCTTTGC TGAA 34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION SEQ ID NO:18:

AGCTTTCAGC AAGAGAACAA TCACCTTCTC CATCG

35

09042488.031698